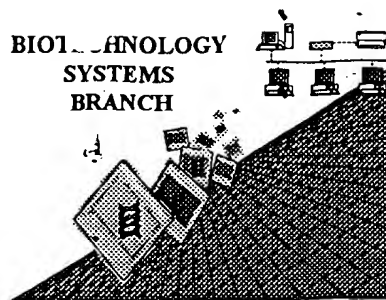


## **RAW SEQUENCE LISTING** **ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



0390  
1023

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/713,601

Source: BLPE

Date Processed by STIC: 10/10/01

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 09/713,601

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics**  
     **Wrapped Aminos**     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2 ☐ **Invalid Line Length**     The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3 ☐ **Misaligned Amino Numbering**     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
  
- 4 ☐ **Non-ASCII**     The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
  
- 5 ☐ **Variable Length**     Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6 ☐ **PatentIn 2.0 "bug"**     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
  
- 7 ☐ **Skipped Sequences (OLD RULES)**     Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
     (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
     (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
     This sequence is intentionally skipped  
  
     Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8 ☐ **Skipped Sequences (NEW RULES)**     Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
     <210> sequence id number  
     <400> sequence id number  
     000
  
- 9 ☐ **Use of n's or Xaa's (NEW RULES)**     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
     Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
     In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10 ☐ **Invalid <213> Response**     Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
  
- 11 ☒ **Use of <220>**     Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
     Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
     (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12 ☐ **PatentIn 2.0 "bug"**     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

## RAW SEQUENCE LISTING

DATE: 10/10/2001

PATENT APPLICATION: US/09/713,601

TIME: 14:08:25

Input Set : A:\04905.ST25.txt

Output Set: N:\CRF3\10102001\I713601.raw

3 <110> APPLICANT: Agarwal, Poonam  
 4 Aizenstein, Brian  
 5 Arco, David  
 6 Atilas, Myrta  
 7 Burris, Deborah  
 8 de Arruda Indig, Monika  
 9 Law, Scott  
 10 Mast, Andrea  
 11 Marshall, David  
 12 Miller, Carolyn  
 13 Oldenberg, Mary  
 14 Rasmussen, Eric  
 15 Schneiders, Jennifer  
 17 <120> TITLE OF INVENTION: Methods and Compositions for Detecting Target Sequences  
 19 <130> FILE REFERENCE: FORS-04905  
 21 <140> CURRENT APPLICATION NUMBER: 09/713,601  
 C--> 22 <141> CURRENT FILING DATE: 2001-09-24  
 24 <150> PRIOR APPLICATION NUMBER: 09/350,309  
 25 <151> PRIOR FILING DATE: 1999-07-09  
 27 <150> PRIOR APPLICATION NUMBER: 09/381,212  
 28 <151> PRIOR FILING DATE: 2000-02-08  
 30 <150> PRIOR APPLICATION NUMBER: 08/823,516  
 31 <151> PRIOR FILING DATE: 1997-03-24  
 33 <150> PRIOR APPLICATION NUMBER: 08/759,038  
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 70 gtctgggcca gcctggccaa gaaggcggaa aaggagggct acgaggtccg catcctcacc 420

Does Not Comply  
 Corrected Diskette Needed

- See Item 11 on Error Summary  
 Sheet, corresponding to  
 error pages 1-5 (attached)

## RAW SEQUENCE LISTING

DATE: 10/10/2001

PATENT APPLICATION: US/09/713,601

TIME: 14:08:25

Input Set : A:\04905.ST25.txt

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## RAW SEQUENCE LISTING

DATE: 10/10/2001

PATENT APPLICATION: US/09/713,601

TIME: 14:08:25

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## RAW SEQUENCE LISTING

DATE: 10/10/2001

PATENT APPLICATION: US/09/713,601

TIME: 14:08:25

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Output Set: N:\CRF3\10102001\I713601.raw

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336 &lt;220&gt; FEATURE:

337 &lt;223&gt; OTHER INFORMATION: Synthetic

339 &lt;400&gt; SEQUENCE: 4

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347 Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala

348 35 40 45

350 Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/713,601

DATE: 10/10/2001

TIME: 14:08:25

Input Set : A:\04905.ST25.txt

Output Set: N:\CRF3\10102001\I713601.raw

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360      100      105      110
362 Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys
363      115      120      125
365 Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp
366      130      135      140
368 Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly
369 145      150      155      160
371 Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro
372      165      170      175
374 Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn
375      180      185      190
377 Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu
378      195      200      205
380 Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu
381      210      215      220
383 Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys
384 225      230      235      240
386 Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val
387      245      250      255
389 Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe
390      260      265      270
392 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
393      275      280      285
395 Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
396      290      295      300
398 Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp
399 305      310      315      320
401 Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro
402      325      330      335
404 Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu
405      340      345      350
407 Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro
408      355      360      365
410 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
411      370      375      380
413 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
414 385      390      395      400
416 Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu
417      405      410      415
419 Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu
420      420      425      430
422 Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly
423      435      440      445

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/713,601

DATE: 10/10/2001

TIME: 14:08:26

Input Set : A:\04905.ST25.txt

Output Set: N:\CRF3\10102001\I713601.raw

L:22 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1051 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1057 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1063 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1071 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1073 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1075 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1077 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1085 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1087 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1091 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1095 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1099 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1103 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1127 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1129 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:1317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:1326 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:1341 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:1344 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:1347 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:1350 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:1353 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:1356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:1362 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:1368 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:1371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:1374 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:1383 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:1386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:1410 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:1419 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:1452 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:1455 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:1461 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:1464 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
61 L:2569 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:2569 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
62 L:2918 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:2918 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
63 L:3375 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:3375 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
7 L:3820 M:258 W: Mandatory Feature missing, <220> FEATURE:



## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/713,601

DATE: 10/10/2001

TIME: 14:08:26

Input Set : A:\04905.ST25.txt

Output Set: N:\CRF3\10102001\I713601.raw

L:3820 M:258 W: Mandatory Feature missing, &lt;223&gt; OTHER INFORMATION:

L:4161 M:258 W: Mandatory Feature missing, &lt;220&gt; FEATURE:

75 L:4161 M:258 W: Mandatory Feature missing, &lt;223&gt; OTHER INFORMATION:

79 L:4378 M:258 W: Mandatory Feature missing, &lt;220&gt; FEATURE:

L:4378 M:258 W: Mandatory Feature missing, &lt;223&gt; OTHER INFORMATION:

L:4807 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:99

L:4831 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:100

L:4849 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:101

L:4867 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:102

L:7058 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:170

L:7094 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:172

L:7130 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174

L:7148 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:175

L:7184 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:177

L:7227 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:179

## STATISTICS SUMMARY

PATENT APPLICATION: US/09/713,601

DATE: 10/10/2001

TIME: 14:08:26

Input Set : A:\04905.ST25.txt

Output Set: N:\CRF3\10102001\I713601.raw

Application Serial Number: US/09/713,601

Alpha or Numeric: Numeric

Application Class:

Application File Date: 09-24-2001

Art Unit: OIPE

Software Application: PatentIn

Total Number of Sequences: 253

Total Nucleotides: 39059

Total Amino Acids: 11901

Number of Errors: 0

Number of Warnings: 71

Number of Corrections: 1

## MESSAGE SUMMARY

258 W: 12 (Mandatory Feature missing)

271 C: 1 (Current Filing Date differs)

341 W: 59 ((46) "n" or "Xaa" used)

09/713,601

Error p. 1

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly  
290 295 300

ctt ctg gaa agc ccc aag gcc gca ctc gag cac cac cac cac cac 960  
Leu Leu Glu Ser Pro Lys Ala Ala Leu Glu His His His His His His  
305 310 315 320

tga 963

<210> 61

<211> 320

<212> PRT

<213> Artificial Sequence



Missing <220> + <223>

<400> 61

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser Gly  
1 5 10 15

Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly  
20 25 30

His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr  
35 40 45

Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu  
50 55 60

Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp  
65 70 75 80

ccc gtc cag ggc acc gcc gcc gac ctc atg aag ctg gct atg gtg aag 2304  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765

ctc ttc ccc agg ctg gag gaa atg ggg gcc agg atg ctc ctt cag gtc 2352  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780

cac aac gag ctg gtc ctc gag gcc cca aaa gag agg gcg gag gcc gtg 2400  
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800

gcc cgg ctg gcc aag gag gtc atg gag ggg gtg tat ccc ctg gcc gtg 2448  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
 805 810 815

ccc ctg gag gtg gag gtg ggg ata ggg gag gac tgg ctc tcc gcc aag 2496  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830

gag tgatag 2505  
 Glu

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<211> 833

<212> PRT

✱ <213> Artificial Sequence  
 Missing <220>+<223>

<400> 66

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 1 5 10 15

&lt;210&gt; 69

&lt;211&gt; 833

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

Missing &lt;220&gt; + &lt;223&gt;

&lt;400&gt; 69

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu

1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys

20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe

35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile

50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly

65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln

85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu

100 105 110

&lt;210&gt; 71

&lt;211&gt; 833

&lt;212&gt; PRT

✱ &lt;213&gt; Artificial Sequence

Missing &lt;220&gt; + &lt;223&gt;

&lt;400&gt; 71

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu

1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys

20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe

35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile

50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly

65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln

85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu

100 105 110

290                      295                      300

gtt gat aaa ctc tat aac tta att gca aac aaa act aag caa aaa aca    960

Val Asp Lys Leu Tyr Asn Leu Ile Ala Asn Lys Thr Lys Gln Lys Thr

305                      310                      315                      320

tta gat gca tgg ttt aaa taa    981

Leu Asp Ala Trp Phe Lys

325

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<212> PRT

*P* <213> Artificial Sequence

*Missing <220> + <223>*

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20                      25                      30

Tyr Gln Phe Leu Thr Ser Ile Arg Leu Arg Asp Gly Ser Pro Leu Arg

35                      40                      45

Asn Arg Lys Gly Glu Ile Thr Ser Ala Tyr Asn Gly Val Phe Tyr Lys

50                      55                      60

Thr Ile His Leu Leu Glu Asn Asp Ile Thr Pro Ile Trp Val Phe Asp

65                      70                      75                      80